

Analysis of Yield Factors in Earliness Related Traits and Yield in Pigeonpea

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ABSTRACT

Pigeonpea productivity is greatly constrained by poor plant ideotype of existing Indian cultivars. Enhancing pigeonpea yield demands a renewed focus on restructuring the ideal plant type by using more efficient approaches like genomic tools. Pigeonpea [*Cajanus cajan* (L.) Millsp.] belongs to the tribe Phaseoleae in the family Leguminosae. *C. cajan* is the only domesticated species sub tribe Cajaninae and has a genome size of 833.07 Mbp. It is a hardy, widely adapted, drought tolerant pulse crop that is cultivated globally on 5.40 million hectares with an average annual production of 4.48 million tonnes. Due to the vast natural genetic variability in local germplasm and the presence of numerous wild relatives, India is considered as the primary center of origin and remains one of the largest pigeonpea producers accounting for 71% (3.88 mha) and 63.39% (2.84 mt) of the global area and production, respectively. Pigeonpea cultivars have a narrow genetic base due to limited utilization of wild pigeonpea species in breeding programs. The breeding efforts aimed at improving pigeonpea led to the development and release of more than 100 improved varieties over the last 50 years in India (Singh et al. 2016). However, the genetic gain from conventional breeding has remained limited over same period of time. This implies toward an urgent need to strengthen pigeonpea breeding programs with the modern genomic tools to improve their efficacy. Notwithstanding the substantial efforts directed towards pigeonpea genetic improvement, the crop productivity has remained near-stagnant over the last several decades. Poor productivity of pigeonpea is due to a range of constraints, of which poor plant type and longer crop duration of existing cultivars are of paramount significance. Improving yield gains in pigeonpea calls for a renewed focus on restructuring the ideal plant type. Also, the development of short duration pigeonpea cultivars could bring significant increment in pigeonpea productivity. In pigeonpea, days to flowering and days to maturity determine earliness and the two traits are important with respect to increasing cropping intensity in rotation systems such as pigeonpea—wheat system.

Plant ideotype breeding intends to deliver crop genotypes that are suitable for modern farming practices and it involves improvement in key traits such as harvest index and mechanical harvesting. In other words, ideotype breeding seeks accumulating favorable QTLs for various component traits in a given genotype. Several plant attributes including plant height, number of branches, pods per plant and synchronous maturity collectively contribute to improved plant architecture. Besides, short-duration cultivars are important in light of the need for increasing cropping efficiency of farming system. Although conventional breeding in pigeonpea has delivered a range of cultivars catering to the demand of wider farming community, remodeling of plant type through deploying modern genomic tools has not yet been started.

This indicated the involvement of additive gene action and potential for development of early maturing genotypes with enhanced seed yield. Correlation study revealed that days to flowering, flowering period and days to maturity recorded significant positive association among themselves. Though, their associations with seed yield per plant were weak in certain genetic backgrounds, otherwise almost non-significant. Thus, correlation studies revealed that selection for earliness will not directly increase productivity. The

possibility of combining components of earliness with yield-promoting alleles was suggested.[1]

The estimated size of the pigeonpea genome packed in its eleven chromosomes is about 853 Mb, which remained untouched by the genomics revolution for a long time [8, 9]. Recently, a large number of simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers have been developed under the Indo-US Agricultural Knowledge Initiative, creating opportunities for a large scale mapping of

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INTRODUCTION

Genetic analysis of five quantitative traits related to earliness and seed yield in chickpea was carried out using eight segregating populations (F2 generations) and their nine parents. Characters included in the study were days to flowering, flowering period, days to maturity, plant height and seed yield per plant. The results showed that no consistency in magnitude of genetic parameters was observed in any cross populations. However, the F2 of P1xP4 exhibited high magnitude of heritability coupled with high genetic advance and GCV for flowering period, days to maturity and plant height and high heritability with moderate genetic advance and GCV for seed yield per plant.

genes and quantitative trait loci (QTLs) for important agronomic traits [2]. Analysis of transcriptome and whole genome sequence using second generation high throughput sequencing technologies have made pigeonpea improvement amenable to molecular breeding [3]. Recently, an inter-specific linkage map of pigeonpea has been developed using 239 genomic SSR markers [4]. However, to our knowledge

there is no published report on a dense intra-specific linkage map or QTL mapping of important agronomic traits in pigeonpea, except for limited studies using RAPD markers for tagging genes for *Fusarium* wilt resistance and plant type [5]. Earlier, SSR markers were used for the genetic diversity analysis of inbred lines and purity assessment of hybrids, but the level of polymorphism detected was very low [6

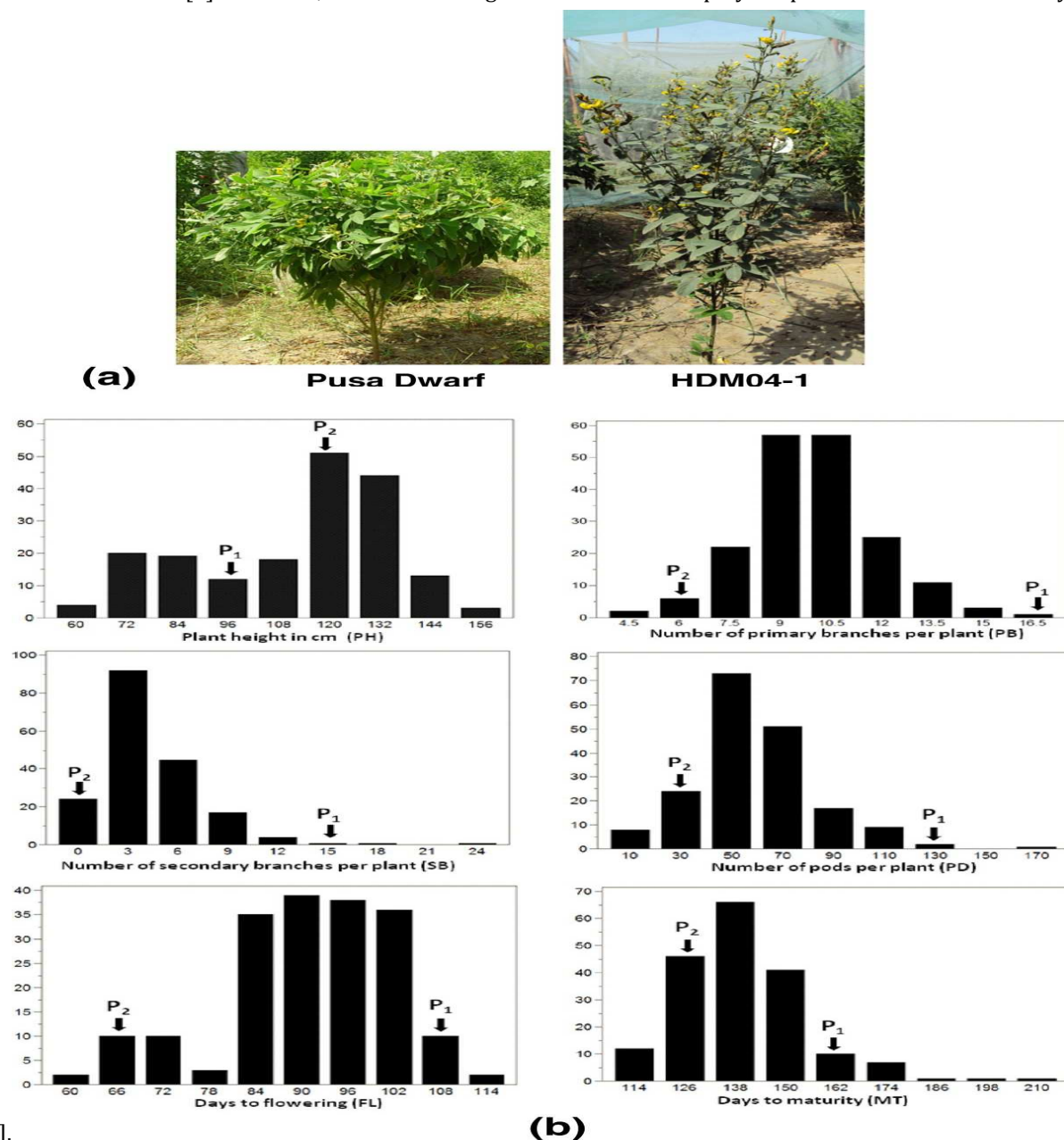


Fig. (a) Field photographs of the parental genotypes Pusa Dwarf and HDM04-1; **(b)** Frequency distribution patterns of six plant architecture and earliness related traits in $F_{2:3}$ population derived from cross between Pusa Dwarf and HDM04-1. P_1 = Pusa Dwarf, P_2 = HDM04-1.

Significant variations were exhibited among genotypes for all assessed qualitative traits ($p < 0.001$) such as growth habit, flower main color, flower streak pattern, pod color, and seed traits. A large proportion of test genotypes (61.9%) were semi-spreading, followed by spreading (26.6%) and compact (11.5%) in growth habits. A majority of the test genotypes (64.9%) had yellow flower color while 16.8% had purple flowers, 13.6% had ivory flowers, and 7.4% had light yellow flowers. A large population of the genotypes (60.5%) had no flower streaks, and the rest of the genotypes had sparse, medium, dense, and uniform coverage streaks at 8.1%, 1.9%, 14.5%, and 15%, respectively. About 48.7% of the genotypes had a green pod color, while 33.9% had a mixed pod color and 7.1% had purple pods. A majority

of the genotypes (76.8%) had a cream seed coat color, while 11% had a brown seed coat color and the rest had gray, orange, and purple seed coat colors. About 70.2% of the test genotypes had a brown seed eye, and 20.7% had a purple seed eye, while the remainder had gray or cream seed eyes. The most common seed shape was square or angular shapes, which were exhibited by 69.3% of the test genotypes.

A population of 186 $F_{2:3}$ lines derived from an intra-specific cross between inbred lines 'Pusa Dwarf' and 'HDM04-1' was used to construct a dense molecular linkage map of 296 genic SNP and SSR markers covering a total adjusted map length of 1520.22 cM for the 11 chromosomes of the pigeonpea genome. This is the first dense intra-specific

linkage map of pigeonpea with the highest genome length coverage. Phenotypic data from the F_{2:3} families were used to identify thirteen QTLs for the six agronomic traits. The proportion of phenotypic variance explained by the individual QTLs ranged from 3.18% to 51.4%. Ten of these QTLs were clustered in just two genomic regions, indicating pleiotropic effects or close genetic linkage. In addition to the main effects, significant epistatic interaction effects were detected between the QTLs for number of pods per plant.[7]

DISCUSSION

The estimated size of the pigeonpea genome packed in its eleven chromosomes is about 853 Mb, which remained untouched by the genomics revolution for a long time [8, 9]. Recently, a large number of simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers have been developed under the Indo-US Agricultural Knowledge Initiative, creating opportunities for a large scale mapping of genes and quantitative trait loci (QTLs) for important agronomic traits [8]. Analysis of transcriptome and whole genome sequence using second generation high throughput sequencing technologies have made pigeonpea improvement amenable to molecular breeding [10]. Recently, an inter-specific linkage map of pigeonpea has been developed using 239 genomic SSR markers [11]. However, to our knowledge there is no published report on a dense intra-specific linkage map or QTL mapping of important agronomic traits in pigeonpea, except for limited studies using RAPD markers for tagging genes for *Fusarium* wilt resistance and plant type [12]. Earlier, SSR markers were used for the genetic diversity analysis of inbred lines and purity assessment of hybrids, but the level of polymorphism detected was very low [13]. The objective of present study was to develop an intra-specific high density framework linkage map of pigeonpea using genic SNP and SSR markers to identify QTLs for plant type and early maturity traits.

CONCLUSION

The work presented here describes the first intra-specific dense molecular linkage map of pigeonpea largely based on genic-SNP markers. It is also the first report on QTL mapping of agronomically important traits in pigeonpea, including plant height, number of branches and pods per plant and maturity time. These results provide strong basis for further investigation on validation and fine mapping of the identified QTLs for plant type and earliness traits, which would help in developing high-yielding early-maturing varieties of pigeonpea for food and nutritional security in the semi-arid tropical and sub-tropical countries.[14]

In the past five decades, constant research has been directed towards yield improvement in pigeonpea resulting in the deployment of several commercially acceptable cultivars in India. Though, the genesis of hybrid technology, the biggest breakthrough, enigma of stagnant productivity still remains unsolved. To sort this productivity disparity, genomic research along with conventional breeding was successfully initiated at ICRISAT. It endowed ample genomic resource providing insight in the pigeonpea genome combating production constraints in a precise and speedy manner. The availability of the draft genome sequence with a large-scale marker resource, oriented the research towards trait mapping for flowering time, determinacy, fertility restoration, yield attributing traits and photo-insensitivity. Defined core and mini-core collection, still eased the pigeonpea breeding being accessible for existing genetic diversity and developing stress resistance. Modern genomic

tools like next-generation sequencing, genome-wide selection helping in the appraisal of selection efficiency is leading towards next-generation breeding, an awaited milestone in pigeonpea genetic enhancement.[15]

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